

**SEQUENCE LISTING**

SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 954 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(iii) FEATURE:

(A) NAME: Alpha 1 chain collagen

10 (B) OTHER INFORMATION: /note="Where  
P=P\*=Hydroxyproline"

5  
10  
15  
20  
25  
30

MAHYITFLCMVLVLLLQNSVLAEDGEVRSSCRTAPTDLVFILDGSYSVGP 50  
ENFEIVKKWLVNITKNFDIGPKFIQVGVVQYSDYPVLEIPLGSYDSGEHL 100  
5 TAAVESILYLGGNTKTGKAIQFALDYLFAKSSRFLTIAVVLTDGKSQDD 150  
VKDAAQAARDSKITLFAIGVGSETEDAELRAIANKPSSTYVFYVEDYIAI 200  
SKIREVMKQKLCEESVCPTRI PVAARDERGF DILLGLDVNKKVKKRIQLS 250  
PKKI KGYEVT SKVDLSELTSNVFPEGLPPSYV FVSTQRFKVKKI WDLWRI 300  
LTIDGRPQIAVTLNGVDKILLFTTT SVINGSQVVT FANPQVKTLFDEGWH 350  
20 QIRLLVTEQDVTLYIDDQQIENKPLHPVLGILINGQTQIGKYSKKEETVQ 400  
FDVQKLRIYCDPEQNNRETACEI PGFCLNGPSDVGSTPAPCICPPGKPLG 450  
QGPKGDPGLPGNPGYPGQPGQDGKPGYQGIAGTPGVPGSPGIQGARGLP 500  
YKGEPGRDGDKGDRGLPGFPGLHGMPSKSGEMGAKGDKGSPGFYGGKKGAK 550  
GEKGNAGFPGLPGPAGEPGRHKG DGLMGSPGFKGEAGSPGAPGDGTRGE 600  
25 PGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQPGTPG 650  
SKGSKGEPGIQGMPGASGLKGE PGATGSPGEPGYMGLPGIQGKKGDKNQ 700  
GEKGIQGGQKGENGRQGI PGQQGIQGHGAKGERGEKGE PGVRGAIGSKGE 750  
SGVDGLMGPA GPKGQPGDPGPQGPGLDGKPGREFSEQFIRQVCTDVIRA 800  
QLPVLLQSGRIRNCDHCLSQHGS PGIPGPPGPIGPEGPRGLPGLPGRDGV 850  
30 PGLVGVPGRPGVRGLKGLPGRNGEKGSQGFYGPGEQGP PGPPGPEGPPGI 900  
SKEGPPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPFRK 950  
GP NY 954

SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME: von Willebrand factor A domain

10

DLVFILDGSYSVGPENFEIVKKWLVNITKNFDIGPKFIQVGVVQYSDYPV 50  
LEIPLGSYDSGEHLTAAVESILYLGNTKTGKAIQFALDYLFKSSRFLT 100  
KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIGVGSETEDAELRAIANKP 150  
SSTYVVFYVEDYIAISKIREVM 171

SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME: Thrombospondin N-terminal-like domain

25

GFDILLGLDVNKKVKKRIQLSPKKIKGYEVTSKVDLSELTSNVFPEGLPP 50  
SYVVFVSTQRFKVKKIWDLWRILTIDGRPQIAVTLNGVDKILLFTTTSVIN 100  
GSQVVTFANPQVKTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPLHPVL 150  
GILINGQTQIGKYSGKEETVQFDVQKLRIYCDP 183

30

SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(ii) MOLECULE TYPE: peptide

5 (iii) FEATURE:

(C) NAME: collagenous domain

(D) OTHER INFORMATION: /note="Where  
P=P\*=Hydroxyproline"

10

0 GKPGLQGPKGDPGLPGNPGYPGQPGQDGKPGYQGIAGTPGVPGSPGIQGA 50  
1 RGLPGYKGEPGRDGDGKDRGLPGFPGLHGMPGSKGEMGAKGDKGSPGFY 100  
2 KKGAKGEKGNAGFPGLPGPAGEPGRHGKDGLMGSPGFKGEAGSPGAPGQD 150  
3 5 GTRGEPGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQ 200  
4 PGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGYMGLPGIQGKKG 250  
5 DKGNQGEKGIQGQKGENGRQGI PGQQGIQGHGAKGERGEKGEPGVRGAI 300  
6 GSKGESGVDGLMGPAKPGQPGDPPGGLDGKPGREFSEQFIRQVCT 350  
7 DVIRAQLPVLLQSGRIRNCDHCLSQHGSPIPGPPGPIGPEGPRGLPGLP 400  
8 20 GRDGVPLVGVPGRPGVRGLKGLPGRNGEKGSQGFYGPGEQGPPEGPPGPE 450  
9 GPPGISKEGPPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARR 500  
10 DPFRRKGPNY 509

25 SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2865 base pairs

(B) TYPE: nucleic acid

(iv) MOLECULE TYPE: cDNA

30 (v) FEATURE: Alpha 1 chain collagen

atggctcactatattacatttctctgcatgggttttgggtgctgcttcttcagaattctgtg 60  
 ttagctgaagatggggaagtaagatcaagttgtcgtactgctccgacagatttagttttc 120  
 atcttagatggctcttatagtgttggcccagaaaactttgaaatagtgaaaaagtggtt 180  
 gtcaatatcacaaaaaactttgacatagggccgaagtttattcaagttggagtgggtcaa 240  
 5 tatagtgactaccctgtgctggagattcctctcgaagctatgattcaggagaacatttg 300  
 acggcagcagtggaatccatactctacttaggaggaaacacaaagacaggaaggccatc 360  
 cagtttgcgctcgattacctttttgccaagtcctcagatttctgactaagatagcagtg 420  
 gtacttacggatggcaaatcccaagatgacgtcaaggatgcagctcaagcagcaagagat 480  
 agtaagataacattatttgctattgggtgttgggttcagaaacagaagatgccgaacttaga 540  
 10 gctattgccaacaagccttctgctacttatgtgttttatgtggaagactatattgcaata 600  
 tccaaaataagggaagtgatgaagcagaaaactttgtgaagaatctgtctgtccaacacga 660  
 attccagtggcagctcgtgatgaaaggggatttgatattcttttaggtttagatgtaaat 720  
 aaaaagggttaagaaaagaatacagctttcaccaaaaaagataaaaggatatgaagtaaca 780  
 tcaaaagttgatttatcagaactcacaaagcaatgttttccagaagggtcttctccatca 840  
 15 tatgtatttgtgtctactcaaagatttaaagtcaagaaaaatttgggatttatggagaata 900  
 ttaactattgatggaaggccacaaatagcagttaccttaaattggtgtggacaaaatctta 960  
 ttatttacaacaaccagcgtaatatgggtcacaagtggttacctttgctaaccctcaa 1020  
 gtttaagacgttgtttgatgaaggctggcaccacaaattcgtctcttagtaacagaacaagat 1080  
 gtgactttgtatattgatgaccaacaaattgaaaacaagcccttacatccagttttaggg 1140  
 20 atcttgatcaatgggcaaacccaaatttgaaaaatattctggaaaagaagaaactgttcag 1200  
 tttgatgtccaaaagttgcaatctactgtgaccacagaacagaacaaccgggagacagca 1260  
 tgtgagattcctggattttgccttaattggtcccagtgatgtaggttcaactccagctccc 1320  
 tgtatttgtcctccgggaaaaccaggacttcaaggccccaaagggtgaccctggactgcct 1380  
 gggaaacctggctaccctggacaacctgggtcaagatggtaagcctggatatcagggaatt 1440  
 25 gcagggaaccaggtgttccaggatctccaggaatacaaggagctcgaggactaccaggt 1500  
 taaaaaggagaaccaggggcgagatgggtgacaaggggtgatcgtggacttctgttttct 1560  
 gggcttcatggcatgccaggatcaaaggggtgaaatgggtgccaaaggagacaaaggatca 1620  
 cctggattttatggcaaaaaggggtgcaaaaggtgaaaaggggaatgctggcttccctggc 1680  
 ctccctggacctgctggagaaccaggaagacatggaaaggatggattaatgggtagtccc 1740  
 30 ggtttcaagggaagcaggatcccctggtgctccggggcaggatggaacacggggagag 1800  
 cctggaatcccaggatttctggaacccaggatataatgggccaaaaggagaaattggg 1860  
 cctccaggacagcaaggaaaaaaggagccccaggatgcctggtttaatgggaagcaat 1920  
 ggctcaccaggccagcctggaacaccgggatctaagggaagcaaagggtgaacctggaatt 1980  
 caagggatgcctggggcttctgggctcaagggaagacaggagcaacgggttccccagga 2040  
 35 gaaccaggatacatgggtttaccgggattcaaggaaaaaagggggacaaaggaaatcaa 2100  
 ggtgaaaaaggtattcaggggtcaaaagggaagaaatggaagacagggaattccaggggcaa 2160  
 cagggaattcaaggccatcatggtgcaaaaggagagagaggtgaaaagggaacctgggt 2220  
 gtccgaggtgccattggatcaaaaggagaatctggggtggatggcttgatggggcccgca 2280  
 ggtcctaaggggcaacctggggatccaggtcctcagggaacccccagggttggatgggaag 2340  
 40 cccggaagagagttttcagaacaatttatcgacaagtttgacagatgtaataagagcc 2400  
 cagctaccagtttacttcagagtggagaattagaaattgtgatcattgcctgtcccaa 2460

File: 0648-5921-US/Final/ Frank/Chiumeow

catggctccccgggtattcctgggccacctgggtccgataggccagagggtcccagagga	2520
ttacctgggtttgccaggaagagatgggtgttcctggattagtgggtgtccctggacgtcca	2580
gggtgtcagaggattaaaaggcctaccaggaagaaatggggaaaaaggagccaagggttt	2640
gggtatcctggagaacaaggctcctcctgggtccccagggtccagagggccctcctggaata	2700
agcaaagaaggtcctccaggagacccagggtctccctggcaaagatggagaccatggaaaa	2760
cctggaatccaaggggcaaccaggccccccaggcatctgcgacccatcactatgttttagt	2820
gtaattgccagaagagatccgttcagaaaaggaccaaactattag	2865

10

[illegible]